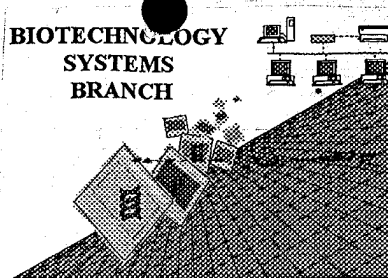


## **RAW SEQUENCE LISTING** **ERROR REPORT**

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



0280

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

09/692,077

Source:

O/PK

Date Processed by STIC:

11/2/2000

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin30help@uspto.gov](mailto:patin30help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

### **Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

**Checker Version 3.0 can be down loaded from the USPTO website at the following address:**

**<http://www.uspto.gov/web/offices/pac/checker>**

invalid format for entire sequence listing 09/692,077 1

Does Not Comply  
Corrected Diskette Needed

<1107 < insert numeric identifier and applicant  
Application Project ~~delete~~ names

~~Application Project~~

<120> Title: Alpha-2B-Adrenergic Receptor Polymorphisms

<130> AppFileReference: 13105

<140> CurrentAppNumber:

<141> CurrentFilingDate: ~~delete~~

<1607 < insert numeric identifier and total number of sequenced figure

Sequence ~~22107 1~~

~~22117 1353~~

~~22127 DNA~~

<213> OrganismName: Homo sapiens

<400> PreSequenceString: 1

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120CGCTCGCTGC GCGCCCTCA GAACCTGTT CTGGTGTGCG TGGCCGCCGC CGACATCCTG  
180GTGGCCACGC TCATCATCCC TTTCTCGCTG GCCAACGAGC TGCTGGGCTA CTGGTACTTC  
240CGGCGCACGT GGTGCGAGGT GTACCTGGCG CTCGACGTGC TCTTCTGCAC CTCGTCCATC  
300GTGCACCTGT GCGCCATCAG CCTGGACCGC TACTGGGCCG TGAGCCGCGC GCTGGAGTAC  
360AACTCCAAGC GCACCCCGCG CCGCATCAAG TGATCATCC TCACTGTGTG GCTCATCGCC  
420GCCGTCACT CGCTGCCGCC CCTCATCTAC AAGGGCGACC AGGGCCCCCA GCCGCGCGGG  
480CGCCCCCAGT GCAAGCTCAA CCAGGAGGCC TGGTACATCC TGGCTCCAG CATCGGATCT  
540TCTTTGCTC CTGCTCAT CATGATCCTT GTCTACCTGC GCATCTACCT GATCGCCAAA  
600CGCAGCAACC GCAGAGTCC CAGGGCCAA GGGGGCCCTG GGCAGGTGA GTCCAAGCAG  
660CCCCGACCCG ACCATGGTGG GGCTTTGGCC TCAGCCAAAC TGCCAGCCCT GGCCTCTGTG  
720ECTTCTGCCA GAGAGTCAA CGGACACTCG AAGTCCACTG GGGAGAAGGA GGAGGGGGAG  
780ACCCCTGAAG ATACTGGGAC CCGGGCCTTG CCACCCAGTT GGGCTGCCCT TCCCAACTCA  
840GGCCAGGGCC AGAAGGAGG TGTGTGTGG GCATCTCCAG AGGATGAAGC TGAAGAGGAG  
900GAAGAGGAGG AGGAGGAGGA GGAAGAGTGT GAACCCAGG CAGTGCCAGT GTCTCCGGCC  
960TCAGCTTGCA GCGCCCGCT GCAGCAGCCA CAGGGCTCCC GGGTGCTGGC CACCCTACGT  
1020GGCCAGGTGC TCCTGGGCAG GGGCGTGGGT GCTATAGGTG GGCAGTGGTG GCGTCGAAGG  
1080GCGCAGCTGA CCCGGGAGAA GCGCTTCACC TTCGTGCTGG CTGTGGTCA TGGCGTTTTT  
1140GTGCTCTGCT GGTTCCTCTT CTCTTCAGC TACAGCCTGG CGCCATCTG CCCGAAGCAC  
1200TGCAAGGTGC CCCATGGCCT CTTCAGTTC TTCTTCTGGA TCGGCTACTG CAACAGCTCA  
1260CTGAACCTG TTATCTACAC CATCTTCAAC CAGGACTTCC GCCGTGCCTT CCGGAGGATC  
1320CTGTGCCGCC CGTGGACCCA GACGGCCTTG TGA

<212> Type: DNA

<211> Length: 1353

SequenceName: Sequence 1

SequenceDescription:

<2107 2

Custom Coding

~~2~~

SequenceName: Sequence 1

~~22117 1344~~

~~22127 DNA~~

~~Sequence~~

~~2~~

<213> OrganismName: Homo sapiens

<400> PreSequenceString: 2

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60TTCTCATTC TCTTTACCAT CTTCGGCAAC GCTCTGGTCA TCTGGCTGT GTTGACCAGC  
120CGCTCGCTGC GCGCCCTCA GAACCTGTT CTGGTGTGCG TGGCCGCCGC CGACATCCTG  
180GTGGCCACGC TCATCATCCC TTTCTCGCTG GCCAACGAGC TGCTGGGCTA CTGGTACTTC  
240CGGCGCACGT GGTGCGAGGT GTACCTGGCG CTCGACGTGC TCTTCTGCAC CTCGTCCATC  
300GTGCACCTGT GCGCCATCAG CCTGGACCGC TACTGGGCCG TGAGCCGCGC GCTGGAGTAC  
360AACTCCAAGC GCACCCCGCG CCGCATCAAG TGATCATCC TCACTGTGTG GCTCATCGCC  
420GCCGTCACT CGCTGCCGCC CCTCATCTAC AAGGGCGACC AGGGCCCCCA GCCGCGCGGG  
480CGCCCCCAGT GCAAGCTCAA CCAGGAGGCC TGGTACATCC TGGCTCCAG CATCGGATCT  
540TCTTTGCTC CTGCTCAT CATGATCCTT GTCTACCTGC GCATCTACCT GATCGCCAAA

60 insert  
120 cumulative  
base totals  
at right  
margin of  
each line

DO NOT use  
upper-case base  
letters in  
new sequence  
header format.  
use lower-case  
letters  
for bases

1353

insert  
cumulative  
base totals  
at right  
margin and  
use lower-case  
letters  
for bases

delete  
totals

delete

09/692,077

2

*Delete*

```
600CGCAGCAACC GCAGAGGTCC CAGGGCCAAG GGGGGGCCTG GGCAGGGTGA GTCCAAGCAG
660CCCCGACCCG ACCATGGTGG GGCTTTGGCC TCAGCCAAAC TGCCAGCCCT GGCCTCTGTG
720GCTTCTGCCA GAGAGGTCAA CGGACACTCG AAGTCCACTG GGGAGAAGGA GGAGGGGGAG
780ACCCCTGAAG ATACTGGGAC CCGGGCCTTG CCACCCAGTT GGGCTGCCCT TCCCAACTCA
840GGCCAGGGCC AGAAGGAGGG TGTTTGTGGG GCATCTCCAG AGGATGAAGC TGAAGAGGAG
900GAGGAGGAGG AGGAAGAGTG TGAACCCCAG GCAGTGCCAG TGTCTCCGGC CTCAGCTTGC
960AGCCCCCCCCG TGCAGCAGCC ACAGGGCTCC CGGGTGCTGG CCACCCTACG TGGCCAGGTG
1020CTCCTGGGCA GGGGCGTGGG TGCTATAGGT GGGCAGTGGT GGCCTCGAAG GGCAGAGCTG
1080ACCCGGGAGA AGCGCTTCAC CTTCGTGCTG GCTGTGGTCA TTGGCGTTTT TGTGCTCTGC
1140TGGTTCCCTT TCTTCTTCAG CTACAGCCTG GGCGCCATCT GCCCGAAGCA CTGCAAGGTG
1200CCCCATGGCC TCTTCCAGTT CTTCTTCTGG ATCGGCTACT GCAACAGCTC ACTGAACCTT
1260GTTATCTACA CCATCTTCAA CCAGGACTTC CGCCGTGCCT TCCGAGGAT CCTGTGCCGC
1320CCGTGGACCC AGACGGCCTG GTGA
```

&lt;212&gt; Type : DNA

&lt;211&gt; Length : 1344

SequenceName : Sequence 2

SequenceDescription :

Custom Codon

Sequence Name : Sequence 2

insert base  
to false and

use  
lower case  
letters.

1344

see next page

22107 7  
22117 450  
22127 PRT  
Sequence

09/692077 3

per sequence rules, use  
three-letter amino

↓ acids and number  
them under  
every 5 amino  
acids.

<213> OrganismName: Homo sapiens

<400> PreSequenceString: ?

MDHQDPYSVQ ATAAIAAAIT FLILFTIFGN ALVILAVLTS RSLRAPQNLF LVSLAAADIL  
60VATLIIPFSL ANELLGYWYF RRTWCEVYLA LDVLFCTSSI VHLCAISLDR YWAVSRALEY  
120NSKRTPRRIK CIILTVWLIA AVISLPPLIY KGDQGPQPRG RPQCKLNQEA WYILASSIGS  
180FFAPCLIMIL VYLRIYLIAK RSNRRGPRAK GGPGQGESHQ PRPDHGGALA SAKLPALASV  
240ASAREVNGHS KSTGEKEEGE TPEDTGTRAL PPSWAALPNS GQGQKEGVCG ASPEDEAESE  
300EEEEEEEEEC EPQAVPVSPA SACSPPLOQP QGSRVLATLR GQVLLGRGVG AIGGQWRRRR  
360AQLTREKRFT FVLAVVIGVF VLCWFPPFFS YSLGAICPKH CKVPHGLFQF FFWIGYCNSS  
420LNPVIYTIFN QDFRAFRRI LCRPWTQTAW

<212> Type: PRT

<211> Length: 450

SequenceName: Sequence 7

SequenceDescription:

450 delete

DO NOT use  
TAB codes  
between amino  
acid nos. Use  
space characters.

a maximum of  
16 amino acids  
per line allowed.

FYI: only three sequences shown as a sample  
of global errors in the entire sequence  
Listing. Please: consult new Sequence  
Rules for acceptable format, and consult  
sample Sequence Listing, attached.

FYI

Please review the

Sequence Listing to ensure that a corresponding explanation is presented in the <220> to  
<223> fields of each sequence which presents at least one n or Xaa.

## Appendix A To Subpart C to Part I—Sample Sequence Listing

&lt;110&gt; Smith, John

Smith, Jane

## &lt;120&gt; Example of a Sequence Listing

&lt;130&gt; 01-00001

&lt;140&gt; US 08/999,999

&lt;141&gt; 1998-02-28

&lt;150&gt; EP 91000000

&lt;151&gt; 1997-12-31

*Consult*

---

---

<160> 2

<170> PatentIn ver. 2.0

<210> 1

<211> 403

<212> DNA

<213> Paramecium aurelia

<220>

<221> CDS

<222> 341..394

<300>

<301> Doe, Richard

<302> Isolation and Characterization of a Gene Encoding a

Protease from Paramecium sp.

<303> Journal of Fictional Genes

<304> 1

<305> 4

<306> 1 - 7

<307> 1988-06-20

<400> 1

ctactctact ctactctcat ctactatctt ctttgatct ctgagctgc ctgagtggta 60

ctcttgagtc ctggagatct ctctctcac atgtgatct cgagactgac cgatagatcg 120

ctgactgact ctgagatagt cgagcccgta cgagaccgt cgagggtgac agagagtggg 180

cgcggtgcgcg cagagcgccg cgccggtgcg cgcgcgagt cgcggtgggc cgcgcgagg 240

ctttcgggc agcgggggcg ctttcggcg cgcgcccgtc cgccctaga cctgagaggt 300

cttctcttcc ctctcttca ctagagaggt ctatatatac atg gtt tca atg ttc 355

Met Val Ser Met Phe

agc ttg tct ttc aaa tgg cct gga ttt tgt ttg ttt gtt tgtttgctc 403

Ser Leu Ser Phe Lys Trp Pro Gly Phe Cys Leu Phe Val

10

15

<210> 2

<211> 18

<212> PRT

<213> *Paramecium aurelia*

<400> 2

Met Val Ser Met Phe Ser Leu Ser Phe Lys Trp Pro Gly Phe Cys Leu

1

5

10

15

Phe Val

ed: May 22, 1998.

A. Lehman,

ant Secretary of Commerce and  
nssloner of Patents and Trademarks.

oc. 98-14194 Filed 5-29-98; 8:45 am]

1 CODE 3510-16-C

identifiers and their accompanying information as shown in the following table. The numeric identifier shall be used only in the "Sequence Listing." The order and presentation of the items of information in the "Sequence Listing" shall conform to the arrangement given below. Each item of information shall begin on a new line and shall begin with the numeric identifier enclosed in angle brackets as shown. The submission of those items of information designated with an "M" is mandatory. The submission of those items of information designated with an "O" is optional. Numeric identifiers <110> through <170> shall only be set forth at the beginning of the "Sequence Listing." The following table illustrates the numeric identifiers.

Numeric Identifier	Definition	Comments and Format	Mandatory (M) or Optional (O)
<110>	Applicant	Preferably max. of 10 names; one name per line; preferable format: Surname, Other Names, and/or Initials.	M
<120>	Title of Invention		M
<130>	File Reference	Personal file reference	M when filed prior to assignment of appl. number
<140>	Current Application Number	Specify as: US 07/999,999 or PCT/US96/99999	M, if available
<141>	Current Filing Date	Specify as: yyyy-mm-dd	M, if available
<150>	Prior Application Number	Specify as: US 07/999,999 or PCT/US96/99999	M, if applicable include priority documents under 35 USC 119 and 120
<151>	Prior Application Filing Date	Specify as: yyyy-mm-dd	M, if applicable
<160>	Number of SEQ ID NOs	Count includes total number of SEQ ID NOs	M
<170>	Software	Name of software used to create the Sequence Listing	O
<210>	SEQ ID NO:#:	Response shall be an integer representing the SEQ ID NO shown	M
<211>	Length	Respond with an integer expressing the number of bases or amino acid residues	M

<212>	Type	Whether presented sequence molecule is DNA, RNA, or PRT (protein). If a nucleotide sequence contains both DNA and RNA fragments, the type shall be "DNA." In addition, the combined DNA/RNA molecule shall be further described in the <220> to <223> feature section.	M
<213>	Organism	Scientific name, i.e. Genus/species, Unknown or Artificial Sequence. In addition, the "Unknown" or "Artificial Sequence" organisms shall be further described in the <220> to <223> feature section.	M
<220>	Feature	Leave blank after <220>. <221-223> provide for a description of points of biological significance in the sequence.	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence; if ORGANISM is "Artificial Sequence" or "Unknown"; if molecule is combined DNA/RNA.
<221>	Name/Key	Provide appropriate identifier for feature, preferably from WIPO Standard ST.25 (1998), Appendix 2, Tables 5 and 6	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence
<222>	Location	Specify location within sequence; where appropriate state number of first and last bases/amino acids	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified

		in feature	base was used in a sequen
<223>	Other Information	Other relevant information; four lines maximum	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence; if ORGANISM is "Artificial Sequence" or "Unknown"; if molecule is combined DNA/RNA.
<300>	Publication Information	Leave blank after <300>	0
<301>	Authors	Preferably max of ten named authors of publication; specify one name per line; preferable format: Surname, Other Names and/or Initials	0
<302>	Title		0
<303>	Journal		0
<304>	Volume		0
<305>	Issue		0
<306>	Pages		0
<307>	Date	Journal date on which data published; specify as yyyy-mm-dd, MMM-yyyy or Season-yyyy	0
<308>	Database Accession Number	Accession number assigned by database including database name	0
<309>	Database Entry Date	Date of entry in database; specify as yyyy-mm-dd or MMM-yyyy	0
<310>	Patent Document Number	Document number; for patent-type citations only. Specify as, for example, US 07/999,999	0

<311>	Patent Filing Date	Document filing date, for patent-type citations only; specify as yyyy-mm-dd	O
<312>	Publication Date	Document publication date, for patent-type citations only; specify as yyyy-mm-dd	O
<313>	Relevant Residues	FROM (position) TO (position)	O
<400>	Sequence	SEQ ID NO should follow the numeric identifier and should appear on the line preceding the actual sequence	M

5. Section 1.824 is revised to read as follows:

1.824 Form and format for nucleotide and/or amino acid sequence submissions in computer readable form.

(a) The computer readable form required by 1.821(e) shall meet the following specifications:

(1) The computer readable form shall contain a single "Sequence Listing" as either a diskette, series of diskettes, or other permissible media outlined in paragraph (c) of this section.

(2) The "Sequence Listing" in paragraph (a) (1) of this section shall be submitted in American Standard Code for Information Interchange (ASCII) text. No other formats shall be allowed.

(3) The computer readable form may be created by any means, such as word processors, nucleotide/amino acid sequence editors or other custom computer programs; however, it shall conform to all specifications detailed in this section.

(4) File compression is acceptable when using diskette media, so long as the compressed file is in a self-extracting format that will decompress on one of the systems described in paragraph (b) of this section.

(5) Page numbering shall not appear within the computer readable form version of the "Sequence Listing" file.

(6) All computer readable forms shall have a label permanently affixed thereto on which has been hand-printed or typed: the name of the applicant, the title of the invention, the date on which the data were recorded on the computer readable form, the operating system used, a reference number, and an application serial number and filing date, if known.

(b) Computer readable form submissions must meet these format requirements:

(1) Computer: IBM PC/XT/AT, or compatibles, or Apple Macintosh;

(2) Operating System: MS-DOS, Unix or Macintosh;